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<110> Gozes, Illana
Brenneman, Douglas E.
Bassan, Merav
Zamostiano, Rachel
The Government of the United States of America
as represented by the Secretary of the
Department of Health and Human Services

<120> Activity Dependent Neurotrophic Factor III (ADNF III)

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<141> 1998-11-06

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<151> 1997-02-07

<150> WO PCT/US98/02485
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<170> PatentIn Ver. 2.0

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 <223> Description of Artificial Sequence:ADNF-9 active
 peptide antigen

<400> 5
 Ser Ala Leu Leu Arg Ser Ile Pro Ala
 1 5

<210> 6
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:ADNF III-8
 active site core peptide, clone 25 sequence (NAP)

<400> 6
 Asn Ala Pro Val Ser Ile Pro Gln
 1 5

<210> 7
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:sense primer
 for amplification of ADNF III cDNA

<400> 7
 tccaatgttc acctgcag

18

<210> 8
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:antisense
 primer (bases 438-455) for amplification of ADNF
 III cDNA

<400> 8
 gctcgttaca gattgtac

18

<210> 9
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:sense primer
 (bases 71-90) for amplification of ADNF III cDNA

<400> 9
 acctgcagca aaacaactat

20

<210> 10
 <211> 88
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:activity
 dependent neurotrophic factor III (ADNF III)
 polypeptide

<220>
 <221> MOD_RES
 <222> (1)..(40)
 <223> Xaa = any amino acid, Xaa at positions 1-40 may be
 present or absent

<220>
 <221> MOD_RES
 <222> (49)..(88)
 <223> Xaa = any amino acid, Xaa at positions 49-88 may be
 present or absent

<400> 10
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Ala Pro Val Ser Ile Pro Gln
 35 40 45

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 50 55 60

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 65 70 75 80

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 85

<210> 11
 <211> 5
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:short hsp60
homolog control peptide

<400> 11

Leu Gly Gly Gly Ser
1 5

<210> 12

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ADNF III
polypeptide

<400> 12

Ser Val Arg Leu Gly Leu Gly Gly Asn Ala Pro Val Ser Ile Pro Gln
1 5 10 15

Gln Ser

<210> 13

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ADNF III
polypeptide; short hsp60 homolog control peptide

<400> 13

Val Leu Gly Gly Gly
1 5

<210> 14

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ADNF III
polypeptide

<400> 14

Val Leu Gly Gly
1

<210> 15

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ADNF III
polypeptide

<400> 15

Val Leu Gly Gly Val
1 5

<210> 16

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ADNF III
polypeptide

<400> 16

Gly Val Leu Gly Gly
1 5

<210> 17

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ADNF III
polypeptide

<400> 17

Leu Gly Leu Gly Gly
1 5

<210> 18

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ADNF III
polypeptide

<400> 18

Ser Val Arg Leu Gly Leu Gly Gly
1 5

<210> 19

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:related to
yeast protein PIF1


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<220>
<221> MOD_RES
<222> (10)
<223> Xaa = unknown
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<210> 20
<211> 13
<212> PRT
<213> Artificial Sequence
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<220>
<221> MOD_RES
<222> (5)
<223> Xaa = unknown
```

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<220>  
<221> MOD_RES  
<222> (8)  
<223> Xaa = unknown
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<220>  
<221> MOD_RES  
<222> (10)  
<223> Xaa = unknown
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<210> 21
<211> 15
<212> PRT
<213> Artificial Sequence
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<400> 21
Cys Val Leu Gly Gly Gly Ser Ala Leu Leu Arg Ser Ile Pro Ala
1 5 10 15

<210> 22
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:peptide
 conjugated through the Cys residue to Sephadex for
 affinity chromatography

<400> 22
 Cys Ser Ala Leu Leu Arg Ser Ile Pro Ala
 1 5 10

<210> 23
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:active peptide
 of ADNF I hsp60-related sequence

<400> 23
 Val Leu Gly Gly Gly Ser Ala Leu Leu Arg Ser Ile Pro Ala
 1 5 10

<210> 24
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:hsp60 homolog
 peptide

<400> 24
 Val Leu Gly Gly Gly Cys Ala Leu Leu Arg Cys Ile Pro Ala
 1 5 10

<210> 25
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:mimic hybrid
 primer

<400> 25
 acctgcagca aaacaactat ttccatccc tcaacagt

38

<210> 26
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:cyclophilin
mRNA upper primer, position 348

<400> 26

atggcacagc aggaaagagc

20

<210> 27

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:cyclophilin
mRNA lower primer

<400> 27

ttgccggagt cgacaatgat

20

<210> 28

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:sequence of p25
clone with structural similarity to active peptide
of ADNF I

<400> 28

Gly Gly Asn Ala Pro Val Ser Ile Pro

1

5

<210> 29

<211> 837

<212> DNA

<213> Homo sapiens

<220>

<223> PCR of human ADNF III cDNA from human
neuroblastoma, sense

<400> 29

cattgggccg acgtgcacatg ctcccgcccg ccatggccgc gggattacct gcagcaaac 60
aactatggag tcaaactctgt aggccagggt tacagtgttg gtcagtcaat gagactgggt 120
ctaggtggca acgcaccagt ttccattcct caacaatctc agtctgtaaa gcagttactt 180
ccaagtggaa acggaaggtc ttatgggctt gggtcagagc agaggtccca ggcaccagca 240
agatactccc tgcagtctgc taatgcctct tctctctcat cgggccagtt aaagtctcct 300
tccctctctc agtcacaggc atccagagtg ttaggtcagt ccagttccaa acctgctgca 360
gctgccacag gccctcccc aggtaacct tctcaactc aaaagtggaa aatatgtaca 420
atctgtaacg agcaatcact agtgccggcg cctgcaggtc gaccatatgg gagagctccc 480

aacgcgttgg atgcatagct tgagtattct atagtgtcac ctaaataget tggcgtaatc 540
 atggtcatag ctgtttcctg tgtgaaattg ttatccgctc acaattccac acaacatacg 600
 aaccggaagc ataaagtgtg aagcctgggg tgcctaataga atgagctaac tcacattaat 660
 tgcgttgccg tcactgcccg ctttccaatc nggaaactgt cgtgccaaact gcattaatga 720
 atcgccaac gcgcggggaa aagcggtttg cgtattgggc gctcttcgcg ttctcgctc 780
 aatgaatccc tgcgctcngt ccttccgntg cggnaacgg tatcactcac tcnaatt 837

<210> 30

<211> 850

<212> DNA

<213> Homo sapiens

<220>

<223> PCR of human ADNF III cDNA from human
neuroblastoma, antisense

<400> 30

atnnatatca agctatgcat ccaacgcgtt gggagctctc ccatatggtc gacctgcagg 60
 cgccgcact agtgattgct cgttacagat tgtacatatt ttccactttt gagttgagga 120
 agtgttacct gggggagggc ctgtggcagc tgcagcaggt ttggaactgg actgacctaa 180
 cactctggat gcctgtgact gagagagggg aggagacttt aactggcccg atgagagaga 240
 agaggcatta gcagactgca gggagtatct tgctgggtgcc tgggacctct gctctgacct 300
 aagcccataa gaccttccgt ttccacttgg aagtaactgc ttacagact gagattgttg 360
 aggaatggaa actggtgcgt tgccacctag acccagtctc attgactgac caaactgta 420
 accctggcct acagatttga ctccatagtt gttttgctgc aggtaatccc gcggccatgg 480
 cgcccgaggag catgcgacgt cgggccaat tgccttata gtgagtcgta ttacaattca 540
 ctggccgtcg ttttacaacg tcgtgactgg gaaaaccctg gcgttaccga acttaatccc 600
 cttgcagcac atcccccttt cgccagctgg cgttaataac gaagaagccc gcaccgatcg 660
 cccttcccaa cagttgcgca gcctgaatgg cgaatggacg cgctgttag cgcgcattaa 720
 accccgcggg tgttgtggtt acgccgcagc gtgaccgcta cacttgccac cccctaacgc 780
 ccgctccttt ccctttcttc cttcctttct cgccacgtcc cccgntttcc ccgtccaact 840
 ctaaatacgg 850

<210> 31

<211> 787

<212> PRT

<213> Mus musculus

<220>

<223> mouse activity dependent neurotrophic factor III
(ADNF III)

<400> 31

Met	Ser	Asn	Val	His	Leu	Gln	Gln	Asn	Asn	Tyr	Gly	Val	Lys	Ser	Val
1				5					10					15	

Gly	Gln	Ser	Tyr	Gly	Val	Gly	Gln	Ser	Val	Arg	Leu	Gly	Leu	Gly	Gly
			20					25					30		

Asn	Ala	Pro	Val	Ser	Ile	Pro	Gln	Gln	Ser	Gln	Ser	Val	Lys	Gln	Leu
		35					40					45			

Leu	Pro	Ser	Gly	Asn	Gly	Arg	Ser	Phe	Gly	Leu	Gly	Ala	Glu	Gln	Arg
	50					55					60				

Pro	Pro	Ala	Ala	Ala	Arg	Tyr	Ser	Leu	Gln	Thr	Ala	Asn	Thr	Ser	Leu
65					70					75					80

Pro	Pro	Gly	Gln	Val	Lys	Ser	Pro	Ser	Val	Ser	Gln	Ser	Gln	Ala	Ser
				85					90					95	

Arg	Val	Leu	Gly	Gln	Ser	Ser	Ser	Lys	Pro	Pro	Pro	Ala	Ala	Thr	Gly
		100						105					110		

Pro	Pro	Pro	Ser	Asn	His	Cys	Ala	Thr	Gln	Lys	Trp	Lys	Ile	Cys	Thr
		115					120					125			

Ile	Cys	Asn	Glu	Leu	Phe	Pro	Glu	Asn	Val	Tyr	Ser	Val	His	Phe	Glu
	130					135					140				

Lys	Glu	His	Lys	Ala	Glu	Lys	Val	Pro	Ala	Val	Ala	Asn	Tyr	Ile	Met
145					150					155					160

Lys	Ile	His	Asn	Phe	Thr	Ser	Lys	Cys	Leu	Tyr	Cys	Asn	Arg	Tyr	Leu
			165						170					175	

Pro	Thr	Asp	Thr	Leu	Leu	Asn	His	Met	Leu	Ile	His	Gly	Leu	Ser	Cys
		180						185					190		

Pro	Tyr	Cys	Arg	Ser	Thr	Phe	Asn	Asp	Val	Glu	Lys	Met	Ala	Ala	His
		195					200					205			

Met	Arg	Met	Val	His	Ile	Asp	Glu	Glu	Met	Gly	Pro	Lys	Thr	Asp	Ser
	210					215					220				

Thr	Leu	Ser	Phe	Asp	Leu	Thr	Leu	Gln	Gln	Gly	Ser	His	Thr	Asn	Ile
225					230					235					240

His	Leu	Leu	Val	Thr	Thr	Tyr	Asn	Leu	Arg	Asp	Ala	Pro	Ala	Glu	Ser
			245						250					255	

Val	Ala	Tyr	His	Ala	Gln	Asn	Asn	Ala	Pro	Val	Pro	Pro	Lys	Pro	Gln
			260					265					270		

Pro	Lys	Val	Gln	Glu	Lys	Ala	Asp	Val	Pro	Val	Lys	Ser	Ser	Pro	Gln
		275					280					285			

Ala	Ala	Val	Pro	Tyr	Lys	Lys	Asp	Val	Gly	Lys	Thr	Leu	Cys	Pro	Leu
		290				295					300				

Cys Phe Ser Ile Leu Lys Gly Pro Ile Ser Asp Ala Leu Ala His His
 305 310 315 320
 Leu Arg Glu Arg His Gln Val Ile Gln Thr Val His Pro Val Glu Lys
 325 330 335
 Lys Leu Thr Tyr Lys Cys Ile His Cys Leu Gly Val Tyr Thr Ser Asn
 340 345 350
 Met Thr Ala Ser Thr Ile Thr Leu His Leu Val His Cys Arg Gly Val
 355 360 365
 Gly Lys Thr Gln Asn Gly Gln Asp Lys Thr Asn Ala Pro Ser Arg Leu
 370 375 380
 Asn Gln Ser Pro Gly Leu Ala Pro Val Lys Arg Thr Tyr Glu Gln Met
 385 390 395 400
 Glu Phe Pro Leu Leu Lys Lys Arg Lys Leu Glu Glu Asp Ala Asp Ser
 405 410 415
 Pro Ser Cys Phe Glu Glu Lys Pro Glu Glu Pro Val Val Leu Ala Leu
 420 425 430
 Asp Pro Lys Gly His Glu Asp Asp Ser Tyr Glu Ala Arg Lys Ser Phe
 435 440 445
 Leu Thr Lys Tyr Phe Asn Lys Gln Pro Tyr Pro Thr Arg Arg Glu Ile
 450 455 460
 Glu Lys Leu Ala Ala Ser Leu Trp Leu Trp Lys Ser Asp Ile Ala Ser
 465 470 475 480
 His Phe Ser Asn Lys Arg Lys Lys Cys Val Arg Asp Cys Glu Lys Tyr
 485 490 495
 Lys Pro Gly Val Leu Leu Gly Phe Asn Met Lys Glu Leu Asn Lys Val
 500 505 510
 Lys His Glu Met Asp Phe Asp Ala Glu Trp Leu Phe Glu Asn His Asp
 515 520 525
 Glu Lys Asp Ser Arg Val Asn Ala Ser Lys Thr Val Asp Lys Lys His
 530 535 540
 Asn Leu Gly Lys Glu Asp Asp Ser Phe Ser Asp Ser Phe Glu His Leu
 545 550 555 560
 Glu Glu Glu Ser Asn Gly Ser Gly Ser Pro Phe Asp Pro Val Phe Glu
 565 570 575
 Val Glu Pro Lys Ile Pro Ser Asp Asn Leu Glu Glu Pro Val Pro Lys
 580 585 590
 Val Ile Pro Glu Gly Ala Leu Glu Ser Glu Lys Leu Asp Gln Lys Glu
 595 600 605
 Glu Glu Glu Glu Glu Glu Glu Glu Asp Gly Ser Lys Tyr Glu Thr Ile
 610 615 620

His Leu Thr Glu Glu Pro Ala Lys Leu Met His Asp Ala Ser Asp Ser
 625 630 635 640
 Glu Val Asp Gln Asp Asp Val Val Glu Trp Lys Asp Gly Ala Ser Pro
 645 650 655
 Ser Glu Ser Gly Pro Gly Ser Gln Gln Ile Ser Asp Phe Glu Asp Asn
 660 665 670
 Thr Cys Glu Met Lys Pro Gly Thr Trp Ser Asp Glu Ser Ser Gln Ser
 675 680 685
 Glu Asp Ala Arg Ser Ser Lys Pro Ala Ala Lys Lys Lys Ala Thr Val
 690 695 700
 Gln Asp Asp Thr Glu Gln Leu Lys Trp Lys Asn Ser Ser Tyr Gly Lys
 705 710 715 720
 Val Glu Gly Phe Trp Ser Lys Asp Gln Ser Gln Trp Glu Asn Ala Ser
 725 730 735
 Glu Asn Ala Glu Arg Leu Pro Asn Pro Gln Ile Glu Trp Gln Asn Ser
 740 745 750
 Thr Ile Asp Ser Glu Asp Gly Glu Gln Phe Asp Ser Met Thr Asp Gly
 755 760 765
 Val Ala Asp Pro Met His Gly Ser Leu Thr Gly Val Lys Leu Ser Ser
 770 775 780
 Gln Gln Ala
 785

<210> 32
 <211> 781
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human activity dependent neurotrophic factor III
 (ADNF III)

<400> 32
 Met Ser Ser Val His Leu Gln Gln Asn Asn Tyr Gly Val Lys Ser Val
 1 5 10 15
 Gly Gln Gly Tyr Ser Val Gly Gln Ser Met Arg Leu Gly Leu Gly Gly
 20 25 30
 Asn Ala Pro Val Ser Ile Pro Gln Gln Ser Gln Ser Val Lys Gln Leu
 35 40 45
 Leu Pro Ser Gly Asn Gly Arg Ser Tyr Gly Leu Gly Ser Glu Gln Arg
 50 55 60
 Ser Gln Ala Pro Ala Arg Tyr Ser Leu Gln Ser Ala Asn Ala Ser Ser
 65 70 75 80
 Leu Ser Ser Gly His Leu Lys Ser Pro Ser Leu Ser His Ser Gln Ala
 85 90 95

Ser Arg Val Leu Gly Gln Ser Ser Ser Lys Pro Ala Ala Ala Ala Thr
 100 105 110
 Gly Pro Pro Pro Gly Asn Thr Ser Ser Thr Gln Lys Trp Lys Ile Cys
 115 120 125
 Thr Ile Cys Asn Glu Leu Phe Pro Glu Asn Val Tyr Ser Val His Phe
 130 135 140
 Glu Lys Glu His Lys Ala Glu Lys Val Pro Ala Val Ala Asn Tyr Ile
 145 150 155 160
 Met Lys Ile His Asn Phe Thr Ser Lys Cys Leu Tyr Cys Asn Arg Tyr
 165 170 175
 Leu Pro Thr Asp Thr Leu Leu Asn His Met Leu Ile His Gly Leu Ser
 180 185 190
 Cys Pro Tyr Cys Arg Ser Thr Phe Asn Asp Val Glu Lys Met Ala Ala
 195 200 205
 His Met Arg Met Val His Ile Asp Glu Glu Met Gly Pro Lys Thr Asp
 210 215 220
 Ser Thr Leu Ser Phe Asp Leu Thr Leu Gln Gln Gly Ser His Thr Asn
 225 230 235 240
 Ile His Leu Leu Val Thr Thr Tyr Asn Leu Arg Asp Ala Pro Ala Glu
 245 250 255
 Ser Val Ala Tyr His Ala Gln Asn Asn Pro Pro Val Pro Pro Lys Pro
 260 265 270
 Gln Pro Lys Val Gln Glu Lys Ala Asp Ile Pro Val Lys Ser Ser Pro
 275 280 285
 Gln Ala Ala Val Pro Tyr Lys Lys Asp Val Gly Lys Thr Leu Cys Pro
 290 295 300
 Leu Cys Phe Ser Ile Leu Lys Gly Pro Ile Ser Asp Ala Leu Ala His
 305 310 315 320
 His Leu Arg Glu Arg His Gln Val Ile Gln Thr Val His Pro Val Glu
 325 330 335
 Lys Lys Leu Thr Tyr Lys Cys Ile His Cys Leu Gly Val Tyr Thr Ser
 340 345 350
 Asn Met Thr Ala Ser Thr Ile Thr Leu His Leu Val His Cys Arg Gly
 355 360 365
 Val Gly Lys Thr Gln Asn Gly Gln Asp Lys Thr Asn Ala Pro Ser Arg
 370 375 380
 Leu Asn Gln Ser Pro Ser Leu Ala Pro Val Lys Arg Thr Tyr Glu Gln
 385 390 395 400
 Met Glu Phe Pro Leu Leu Lys Lys Arg Lys Leu Asp Asp Asp Ser Asp
 405 410 415

Ser Pro Ser Phe Phe Glu Glu Lys Pro Glu Glu Pro Val Val Leu Ala
 420 425 430
 Leu Asp Pro Lys Gly His Glu Asp Asp Ser Tyr Glu Ala Arg Lys Ser
 435 440 445
 Phe Leu Thr Lys Tyr Phe Asn Lys Gln Pro Tyr Pro Thr Arg Arg Glu
 450 455 460
 Ile Glu Lys Leu Ala Ala Ser Leu Trp Leu Trp Lys Ser Asp Ile Ala
 465 470 475 480
 Ser His Phe Ser Asn Lys Arg Lys Lys Cys Val Arg Asp Cys Glu Lys
 485 490 495
 Tyr Lys Pro Gly Val Leu Leu Gly Phe Asn Met Lys Glu Leu Asn Lys
 500 505 510
 Val Lys His Glu Met Asp Phe Asp Ala Glu Trp Leu Phe Glu Asn His
 515 520 525
 Asp Glu Lys Asp Ser Arg Val Asn Ala Ser Lys Thr Ala Asp Lys Lys
 530 535 540
 Leu Asn Leu Gly Lys Glu Asp Asp Ser Ser Ser Asp Ser Phe Glu Asn
 545 550 555 560
 Leu Glu Glu Glu Ser Asn Glu Ser Gly Ser Pro Phe Asp Pro Val Phe
 565 570 575
 Glu Val Glu Pro Lys Ile Ser Asn Asp Asn Pro Glu Glu His Val Leu
 580 585 590
 Lys Val Ile Pro Glu Asp Ala Ser Glu Ser Glu Glu Lys Leu Asp Gln
 595 600 605
 Lys Glu Asp Gly Ser Lys Tyr Glu Thr Ile His Leu Thr Glu Glu Pro
 610 615 620
 Thr Lys Leu Met His Asn Ala Ser Asp Ser Glu Val Asp Gln Asp Asp
 625 630 635 640
 Val Val Glu Trp Lys Asp Gly Ala Ser Pro Ser Glu Ser Gly Pro Gly
 645 650 655
 Ser Gln Gln Val Ser Asp Phe Glu Asp Asn Thr Cys Glu Met Lys Pro
 660 665 670
 Gly Thr Trp Ser Asp Glu Ser Ser Gln Ser Glu Asp Ala Arg Ser Ser
 675 680 685
 Lys Pro Ala Ala Lys Lys Lys Ala Thr Met Gln Gly Asp Arg Glu Gln
 690 695 700
 Leu Lys Trp Lys Asn Ser Ser Tyr Gly Lys Val Glu Gly Phe Trp Ser
 705 710 715 720
 Lys Asp Gln Ser Gln Trp Lys Asn Ala Ser Glu Asn Asp Glu Arg Leu
 725 730 735

Ser Asn Pro Gln Ile Glu Trp Gln Asn Ser Thr Ile Asp Ser Glu Asp
 740 745 750

Gly Glu Gln Phe Asp Asn Met Thr Asp Gly Val Thr Glu Pro Met His
 755 760 765

Gly Ser Leu Ala Gly Val Lys Leu Ser Ser Gln Gln Ala
 770 775 780

<210> 33
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:ADNF III
 polypeptide

<400> 33
 Gly Gly Asn Ala Pro Val Ser Ile Pro Gln
 1 5 10

<210> 34
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:ADNF III
 polypeptide

<400> 34
 Leu Gly Gly Asn Ala Pro Val Ser Ile Pro Gln Gln Ser
 1 5 10

<210> 35
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:ADNF III
 polypeptide

<400> 35
 Leu Gly Leu Gly Gly Asn Ala Pro Val Ser Ile Pro Gln Gln Ser
 1 5 10 15

<210> 36
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:ADNF-9 active
 peptide adsorbed onto bovine serum albumin (BSA)
 as antigen

<400> 36
 Ser Ala Leu Leu Arg Ser Ile Pro Ala
 1 5

<210> 37
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:ADNF
 I/PIF1-related sequence

<400> 37
 Ile Gln Leu Glu Thr Glu Ile Gln Glu Lys Gln Ile Ile
 1 5 10

<210> 38
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:cyclophilin
 mRNA mimic primer

<400> 38
 atggcacagg aggaaagagc aatgcaggca aagacacc

38

<210> 39
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:neuropeptide
 cleavage site

<400> 39
 Lys Lys Arg Lys
 1

<210> 40
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:neuropeptide
 cleavage site

<400> 40
 Lys Arg Lys Lys
 1

<210> 41
 <211> 800
 <212> PRT
 <213> Homo sapiens

<220>
 <221> PEPTIDE
 <222> (1)..(800)
 <223> translation of H3' human ADNF III cDNA clone

<400> 41
 Met Val Asn Arg Leu Ser Ile Pro Lys Pro Asn Leu Asn Ser Thr Gly
 1 5 10 15
 Val Asn Met Met Ser Ser Val His Leu Gln Gln Asn Asn Tyr Gly Val
 20 25 30
 Lys Ser Val Gly Gln Gly Tyr Ser Val Gly Gln Ser Met Arg Leu Gly
 35 40 45
 Leu Gly Gly Asn Ala Pro Val Ser Ile Pro Gln Gln Ser Gln Ser Val
 50 55 60
 Lys Gln Leu Leu Pro Ser Gly Asn Gly Arg Ser Tyr Gly Leu Gly Ser
 65 70 75 80
 Glu Gln Arg Ser Gln Ala Pro Ala Arg Tyr Ser Leu Gln Ser Ala Asn
 85 90 95
 Ala Ser Ser Leu Ser Ser Gly His Leu Lys Ser Pro Ser Leu Ser His
 100 105 110
 Ser Gln Ala Ser Arg Val Leu Gly Gln Ser Ser Ser Lys Pro Ala Ala
 115 120 125
 Ala Ala Thr Gly Pro Pro Pro Gly Asn Thr Ser Ser Thr Gln Lys Trp
 130 135 140
 Lys Ile Cys Thr Ile Cys Asn Glu Leu Phe Pro Glu Asn Val Tyr Ser
 145 150 155 160
 Val His Phe Glu Lys Glu His Lys Ala Glu Lys Val Pro Ala Val Ala
 165 170 175
 Asn Tyr Ile Met Lys Ile His Asn Phe Thr Ser Lys Cys Leu Tyr Cys
 180 185 190
 Asn Arg Tyr Leu Pro Thr Asp Thr Leu Leu Asn His Met Leu Ile His
 195 200 205
 Gly Leu Ser Cys Pro Tyr Cys Arg Ser Thr Phe Asn Asp Val Glu Lys
 210 215 220
 Met Ala Ala His Met Arg Met Val His Ile Asp Glu Glu Met Gly Pro
 225 230 235 240
 Lys Thr Asp Ser Thr Leu Ser Phe Asp Leu Thr Leu Gln Gln Gly Ser
 245 250 255
 His Thr Asn Ile His Leu Leu Val Thr Thr Tyr Asn Leu Arg Asp Ala
 260 265 270

Pro Ala Glu Ser Val Ala Tyr His Ala Gln Asn Asn Pro Pro Val Pro
 275 280 285
 Pro Lys Pro Gln Pro Lys Val Gln Glu Lys Ala Asp Ile Pro Val Lys
 290 295 300
 Ser Ser Pro Gln Ala Ala Val Pro Tyr Lys Lys Asp Val Gly Lys Thr
 305 310 315 320
 Leu Cys Pro Leu Cys Phe Ser Ile Leu Lys Gly Pro Ile Ser Asp Ala
 325 330 335
 Leu Ala His His Leu Arg Glu Arg His Gln Val Ile Gln Thr Val His
 340 345 350
 Pro Val Glu Lys Lys Leu Thr Tyr Lys Cys Ile His Cys Leu Gly Val
 355 360 365
 Tyr Thr Ser Asn Met Thr Ala Ser Thr Ile Thr Leu His Leu Val His
 370 375 380
 Cys Arg Gly Val Gly Lys Thr Gln Asn Gly Gln Asp Lys Thr Asn Ala
 385 390 395 400
 Pro Ser Arg Leu Asn Gln Ser Pro Ser Leu Ala Pro Val Lys Arg Thr
 405 410 415
 Tyr Glu Gln Met Glu Phe Pro Leu Leu Lys Lys Arg Lys Leu Asp Asp
 420 425 430
 Asp Ser Asp Ser Pro Ser Phe Phe Glu Glu Lys Pro Glu Glu Pro Val
 435 440 445
 Val Leu Ala Leu Asp Pro Lys Gly His Glu Asp Asp Ser Tyr Glu Ala
 450 455 460
 Arg Lys Ser Phe Leu Thr Lys Tyr Phe Asn Lys Gln Pro Tyr Pro Thr
 465 470 475 480
 Arg Arg Glu Ile Glu Lys Leu Ala Ala Ser Leu Trp Leu Trp Lys Ser
 485 490 495
 Asp Ile Ala Ser His Phe Ser Asn Lys Arg Lys Lys Cys Val Arg Asp
 500 505 510
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 Glu Asn His Asp Glu Lys Asp Ser Arg Val Asn Ala Ser Lys Thr Ala
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 Asp Lys Lys Leu Asn Leu Gly Lys Glu Asp Asp Ser Ser Ser Asp Ser
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Pro Val Phe Glu Val Glu Pro Lys Ile Ser Asn Asp Asn Pro Glu Glu
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 His Val Leu Lys Val Ile Pro Glu Asp Ala Ser Glu Ser Glu Glu Lys
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 Leu Asp Gln Lys Glu Asp Gly Ser Lys Tyr Glu Thr Ile His Leu Thr
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 Glu Glu Pro Thr Lys Leu Met His Asn Ala Ser Asp Ser Glu Val Asp
 645 650 655
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 Gly Pro Gly Ser Gln Gln Val Ser Asp Phe Glu Asp Asn Thr Cys Glu
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 Met Lys Pro Gly Thr Trp Ser Asp Glu Ser Ser Gln Ser Glu Asp Ala
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 Lys Leu Ile His Met Val Val
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 Ser Leu Pro Ser Gln Gln Met Val Asn Arg Leu Ser Ile Pro Lys Pro
 20 25 30

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 Asn Leu Asn Ser Thr Gly Val Asn Met Met Ser Asn Val His Leu Gln
 35 40 45

caa aac aac tat gga gtc aaa tct gtg ggc cag agc tat ggt gtt ggc 192
 Gln Asn Asn Tyr Gly Val Lys Ser Val Gly Gln Ser Tyr Gly Val Gly
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cag tca gtg agg ctg gga cta ggt ggc aat gct cca gtt tcc atc cct 240
 Gln Ser Val Arg Leu Gly Leu Gly Gly Asn Ala Pro Val Ser Ile Pro
 65 70 75 80

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 Gln Gln Ser Gln Ser Val Lys Gln Leu Leu Pro Ser Gly Asn Gly Arg
 85 90 95

tct ttt ggg cta ggt gct gag cag agg ccc cca gca gca gcc agg tac 336
 Ser Phe Gly Leu Gly Ala Glu Gln Arg Pro Pro Ala Ala Ala Arg Tyr
 100 105 110

tcc ctg cag act gcc aac acc tct cta ccc cca ggc caa gtg aag tct 384
 Ser Leu Gln Thr Ala Asn Thr Ser Leu Pro Pro Gly Gln Val Lys Ser
 115 120 125

ccc tct gtg tct cag tca cag gca tct aga gta tta ggt cag tcc agt 432
 Pro Ser Val Ser Gln Ser Gln Ala Ser Arg Val Leu Gly Gln Ser Ser
 130 135 140

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 Ser Lys Pro Pro Pro Ala Ala Thr Gly Pro Pro Pro Ser Asn His Cys
 145 150 155 160

gcc act cag aag tgg aaa atc tgt aca atc tgt aac gag ctt ttc cct 528
 Ala Thr Gln Lys Trp Lys Ile Cys Thr Ile Cys Asn Glu Leu Phe Pro
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 Glu Asn Val Tyr Ser Val His Phe Glu Lys Glu His Lys Ala Glu Lys
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Val Pro Ala Val Ala Asn Tyr Ile Met Lys Ile His Asn Phe Thr Ser	
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Lys Cys Leu Tyr Cys Asn Arg Tyr Leu Pro Thr Asp Thr Leu Leu Asn	
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His Met Leu Ile His Gly Leu Ser Cys Pro Tyr Cys Arg Ser Thr Phe	
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Asn Asp Val Glu Lys Met Ala Ala His Met Arg Met Val His Ile Asp	
245 250 255	
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Glu Glu Met Gly Pro Lys Thr Asp Ser Thr Leu Ser Phe Asp Leu Thr	
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Ile Gln Thr Val His Pro Val Glu Lys Lys Leu Thr Tyr Lys Cys Ile	
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His Cys Leu Gly Val Tyr Thr Ser Asn Met Thr Ala Ser Thr Ile Thr	
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ctg cat cta gtc cac tgc agg ggt gtt gga aaa acc cag aat ggc cag	1248
Leu His Leu Val His Cys Arg Gly Val Gly Lys Thr Gln Asn Gly Gln	
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gac aag aca aac gca cct tct cgg ctc aat cag tct cca ggc ctg gcc	1296
Asp Lys Thr Asn Ala Pro Ser Arg Leu Asn Gln Ser Pro Gly Leu Ala	
420 425 430	

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Pro	Val	Lys	Arg	Thr	Tyr	Glu	Gln	Met	Glu	Phe	Pro	Leu	Leu	Lys	Lys	
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cgg	aag	ctg	gag	gag	gat	gct	gat	tcc	cct	agc	tgc	ttt	gaa	gag	aag	1392
Arg	Lys	Leu	Glu	Glu	Asp	Ala	Asp	Ser	Pro	Ser	Cys	Phe	Glu	Glu	Lys	
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cca	gaa	gag	cct	gtt	gtt	tta	gct	tta	gac	ccc	aag	ggt	cat	gaa	gat	1440
Pro	Glu	Glu	Pro	Val	Val	Leu	Ala	Leu	Asp	Pro	Lys	Gly	His	Glu	Asp	
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gat	tct	tat	gag	gct	agg	aaa	agc	ttt	ctc	aca	aag	tac	ttc	aac	aaa	1488
Asp	Ser	Tyr	Glu	Ala	Arg	Lys	Ser	Phe	Leu	Thr	Lys	Tyr	Phe	Asn	Lys	
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cag	ccc	tat	ccc	acc	agg	aga	gaa	att	gag	aag	tta	gct	gcc	agt	cta	1536
Gln	Pro	Tyr	Pro	Thr	Arg	Arg	Glu	Ile	Glu	Lys	Leu	Ala	Ala	Ser	Leu	
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tgg	cta	tgg	aag	agt	gac	att	gcc	tcc	cat	ttc	agt	aac	aag	agg	aag	1584
Trp	Leu	Trp	Lys	Ser	Asp	Ile	Ala	Ser	His	Phe	Ser	Asn	Lys	Arg	Lys	
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Lys	Cys	Val	Arg	Asp	Cys	Glu	Lys	Tyr	Lys	Pro	Gly	Val	Leu	Leu	Gly	
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Phe	Asn	Met	Lys	Glu	Leu	Asn	Lys	Val	Lys	His	Glu	Met	Asp	Phe	Asp	
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Ala	Glu	Trp	Leu	Phe	Glu	Asn	His	Asp	Glu	Lys	Asp	Ser	Arg	Val	Asn	
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gct	agc	aag	act	gtt	gac	aaa	aag	cat	aac	ctt	ggg	aaa	gaa	gat	gat	1776
Ala	Ser	Lys	Thr	Val	Asp	Lys	Lys	His	Asn	Leu	Gly	Lys	Glu	Asp	Asp	
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Ser	Phe	Ser	Asp	Ser	Phe	Glu	His	Leu	Glu	Glu	Glu	Ser	Asn	Gly	Ser	
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Gly	Ser	Pro	Phe	Asp	Pro	Val	Phe	Glu	Val	Glu	Pro	Lys	Ile	Pro	Ser	
	610					615					620					
gat	aat	tta	gag	gag	cct	gta	ccg	aag	gtt	att	ccg	gaa	ggt	gct	ttg	1920
Asp	Asn	Leu	Glu	Glu	Pro	Val	Pro	Lys	Val	Ile	Pro	Glu	Gly	Ala	Leu	
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gaa	tct	gag	aag	cta	gac	caa	aaa	gag	gag	gag	gag	gag	gag	gag	gag	1968
Glu	Ser	Glu	Lys	Leu	Asp	Gln	Lys	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	
				645					650					655		
gag	gat	ggt	tca	aaa	tat	gaa	act	atc	cat	ttg	act	gag	gaa	cca	gcc	2016
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Gln Asn Asn Tyr Gly Val Lys Ser Val Gly Gln Ser Tyr Gly Val Gly
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Gln Ser Val Arg Leu Gly Leu Gly Gly Asn Ala Pro Val Ser Ile Pro
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 Ser Leu Gln Thr Ala Asn Thr Ser Leu Pro Pro Gly Gln Val Lys Ser
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 130 135 140
 Ser Lys Pro Pro Pro Ala Ala Thr Gly Pro Pro Pro Ser Asn His Cys
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 Ala Thr Gln Lys Trp Lys Ile Cys Thr Ile Cys Asn Glu Leu Phe Pro
 165 170 175
 Glu Asn Val Tyr Ser Val His Phe Glu Lys Glu His Lys Ala Glu Lys
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 Val Pro Ala Val Ala Asn Tyr Ile Met Lys Ile His Asn Phe Thr Ser
 195 200 205
 Lys Cys Leu Tyr Cys Asn Arg Tyr Leu Pro Thr Asp Thr Leu Leu Asn
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 His Met Leu Ile His Gly Leu Ser Cys Pro Tyr Cys Arg Ser Thr Phe
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ggt cag tca atg aga ctg ggt cta ggt ggc aac gca cca gtt tcc att 192
 Gly Gln Ser Met Arg Leu Gly Leu Gly Gly Asn Ala Pro Val Ser Ile
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 65 70 75 80

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 Arg Ser Tyr Gly Leu Gly Ser Glu Gln Arg Ser Gln Ala Pro Ala Arg
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Lys Ser Pro Ser Leu Ser Gln Ser Gln Ala Ser Arg Val Leu Gly Gln	
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Thr Ser Lys Cys Leu Tyr Cys Asn Arg Tyr Leu Pro Thr Asp Thr Leu	
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Leu Asn His Met Leu Ile His Gly Leu Ser Cys Pro Tyr Cys Arg Ser	
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Thr Phe Asn Asp Val Glu Lys Met Ala Ala His Met Arg Met Val His	
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Ile Asp Glu Glu Met Gly Pro Lys Thr Asp Ser Thr Leu Ser Phe Asp	
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Lys Lys Asp Val Gly Lys Thr Leu Cys Pro Leu Cys Phe Ser Ile Leu	
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Ile Thr Leu His Leu Val His Cys Arg Gly Val Gly Lys Thr Gln Asn	
385 390 395 400	
ggc cag gat aag aca aat gca ccc tct cgg ctt aat cag tct cca agt	1248
Gly Gln Asp Lys Thr Asn Ala Pro Ser Arg Leu Asn Gln Ser Pro Ser	
405 410 415	
ctg gca cct gtg aag cgc act tac gag caa atg gaa ttt ccc tta ctg	1296
Leu Ala Pro Val Lys Arg Thr Tyr Glu Gln Met Glu Phe Pro Leu Leu	
420 425 430	
aaa aaa cga aag tta gat gat gat agt gat tca ccc agc ttc ttt gaa	1344
Lys Lys Arg Lys Leu Asp Asp Asp Ser Asp Ser Pro Ser Phe Phe Glu	
435 440 445	
gag aag cct gaa gag cct gtt gtt tta gct tta gac ccc aag ggt cat	1392
Glu Lys Pro Glu Glu Pro Val Val Leu Ala Leu Asp Pro Lys Gly His	
450 455 460	
gaa gat gat tcc tat gaa gcc agg aaa agc ttt cta aca aag tat ttc	1440
Glu Asp Asp Ser Tyr Glu Ala Arg Lys Ser Phe Leu Thr Lys Tyr Phe	
465 470 475 480	
aac aaa cag ccc tat ccc acc agg aga gaa att gag aag cta gca gcc	1488
Asn Lys Gln Pro Tyr Pro Thr Arg Arg Glu Ile Glu Lys Leu Ala Ala	
485 490 495	
agt tta tgg tta tgg aag agt gac atc gct tcc cat ttt agt aac aaa	1536
Ser Leu Trp Leu Trp Lys Ser Asp Ile Ala Ser His Phe Ser Asn Lys	
500 505 510	
agg aag aag tgt gtc cgt gat tgt gaa aag tac aag cct ggc gtg ttg	1584
Arg Lys Lys Cys Val Arg Asp Cys Glu Lys Tyr Lys Pro Gly Val Leu	
515 520 525	
ctg ggg ttt aac atg aaa gaa tta aat aaa gtc aag cat gag atg gat	1632
Leu Gly Phe Asn Met Lys Glu Leu Asn Lys Val Lys His Glu Met Asp	
530 535 540	
ttt gat gct gag tgg cta ttt gaa aat cat gat gag aag gat tcc aga	1680
Phe Asp Ala Glu Trp Leu Phe Glu Asn His Asp Glu Lys Asp Ser Arg	
545 550 555 560	
gtc aat gct agt aag act gct gac aaa aag ctc aac ctt ggg aag gaa	1728
Val Asn Ala Ser Lys Thr Ala Asp Lys Lys Leu Asn Leu Gly Lys Glu	
565 570 575	
gat gac agt tcc tca gac agt ttt gaa aat ttg gaa gaa gaa tcc aat	1776
Asp Asp Ser Ser Ser Asp Ser Phe Glu Asn Leu Glu Glu Glu Ser Asn	
580 585 590	

gaa agt ggt agc cct ttt gac cct gtt ttt gaa gtt gaa cct aaa atc 1824
 Glu Ser Gly Ser Pro Phe Asp Pro Val Phe Glu Val Glu Pro Lys Ile
 595 600 605

 tct aac gat aac cca gag gaa cat gta ctg aag gta att cct gag gat 1872
 Ser Asn Asp Asn Pro Glu Glu His Val Leu Lys Val Ile Pro Glu Asp
 610 615 620

 gct tca gaa tct gag gag aag cta gac caa aaa gag gat ggt tca aaa 1920
 Ala Ser Glu Ser Glu Glu Lys Leu Asp Gln Lys Glu Asp Gly Ser Lys
 625 630 635 640

 tac gaa act att cat ttg act gag gaa cca acc aaa cta atg cac aat 1968
 Tyr Glu Thr Ile His Leu Thr Glu Glu Pro Thr Lys Leu Met His Asn
 645 650 655

 gca tct gat agt gag gtt gac caa gac gat gtt gtt gag tgg aaa gac 2016
 Ala Ser Asp Ser Glu Val Asp Gln Asp Asp Val Val Glu Trp Lys Asp
 660 665 670

 ggt gct tct cca tct gag agt ggg cct gga tcc caa caa gtg tca gac 2064
 Gly Ala Ser Pro Ser Glu Ser Gly Gly Pro Gly Ser Gln Gln Val Ser Asp
 675 680 685

 ttt gag gac aat acc tgc gaa atg aaa cca gga acc tgg tct gac gag 2112
 Phe Glu Asp Asn Thr Cys Glu Met Lys Pro Gly Thr Trp Ser Asp Glu
 690 695 700

 tct tcc caa agc gaa gat gca agg agc agt aag cca gct gcc aaa aaa 2160
 Ser Ser Gln Ser Glu Asp Ala Arg Ser Ser Lys Pro Ala Ala Lys Lys
 705 710 715 720

 aaa ggc tac cat gca agg tga 2181
 Lys Gly Tyr His Ala Arg
 725

<210> 57

<211> 726

<212> PRT

<213> Homo sapiens

<400> 57

Arg Ser Leu Pro Ser Gln Gln Met Val Asn Arg Leu Ser Ile Pro Lys
 1 5 10 15

Pro Asn Leu Asn Ser Thr Gly Val Asn Met Met Ser Ser Val His Leu
 20 25 30

Gln Gln Asn Asn Tyr Gly Val Lys Ser Val Gly Gln Gly Tyr Ser Val
 35 40 45

Gly Gln Ser Met Arg Leu Gly Leu Gly Gly Asn Ala Pro Val Ser Ile
 50 55 60

Pro Gln Gln Ser Gln Ser Val Lys Gln Leu Leu Pro Ser Gly Asn Gly
 65 70 75 80

Arg Ser Tyr Gly Leu Gly Ser Glu Gln Arg Ser Gln Ala Pro Ala Arg
 85 90 95

Tyr Ser Leu Gln Ser Ala Asn Ala Ser Ser Leu Ser Ser Gly Gln Leu
 100 105 110
 Lys Ser Pro Ser Leu Ser Gln Ser Gln Ala Ser Arg Val Leu Gly Gln
 115 120 125
 Ser Ser Ser Lys Pro Ala Ala Ala Ala Thr Gly Pro Pro Pro Gly Asn
 130 135 140
 Thr Ser Ser Thr Gln Lys Trp Lys Ile Cys Thr Ile Cys Asn Glu Leu
 145 150 155 160
 Phe Pro Glu Asn Val Tyr Ser Val His Phe Glu Lys Glu His Lys Ala
 165 170 175
 Glu Lys Val Pro Ala Val Ala Asn Tyr Ile Met Lys Ile His Asn Phe
 180 185 190
 Thr Ser Lys Cys Leu Tyr Cys Asn Arg Tyr Leu Pro Thr Asp Thr Leu
 195 200 205
 Leu Asn His Met Leu Ile His Gly Leu Ser Cys Pro Tyr Cys Arg Ser
 210 215 220
 Thr Phe Asn Asp Val Glu Lys Met Ala Ala His Met Arg Met Val His
 225 230 235 240
 Ile Asp Glu Glu Met Gly Pro Lys Thr Asp Ser Thr Leu Ser Phe Asp
 245 250 255
 Leu Thr Leu Gln Gln Gly Ser His Thr Asn Ile His Leu Leu Val Thr
 260 265 270
 Thr Tyr Asn Leu Arg Asp Ala Pro Ala Glu Ser Val Ala Tyr His Ala
 275 280 285
 Gln Asn Asn Pro Pro Val Pro Pro Lys Pro Gln Pro Lys Val Gln Glu
 290 295 300
 Lys Ala Asp Ile Pro Val Lys Ser Ser Pro Gln Ala Ala Val Pro Tyr
 305 310 315 320
 Lys Lys Asp Val Gly Lys Thr Leu Cys Pro Leu Cys Phe Ser Ile Leu
 325 330 335
 Lys Gly Pro Ile Ser Asp Ala Leu Ala His His Leu Arg Glu Arg His
 340 345 350
 Gln Val Ile Gln Thr Val His Pro Val Glu Lys Lys Leu Thr Tyr Lys
 355 360 365
 Cys Ile His Cys Leu Gly Val Tyr Thr Ser Asn Met Thr Ala Ser Thr
 370 375 380
 Ile Thr Leu His Leu Val His Cys Arg Gly Val Gly Lys Thr Gln Asn
 385 390 395 400
 Gly Gln Asp Lys Thr Asn Ala Pro Ser Arg Leu Asn Gln Ser Pro Ser
 405 410 415

Leu Ala Pro Val Lys Arg Thr Tyr Glu Gln Met Glu Phe Pro Leu Leu
 420 425 430
 Lys Lys Arg Lys Leu Asp Asp Asp Ser Asp Ser Pro Ser Phe Phe Glu
 435 440 445
 Glu Lys Pro Glu Glu Pro Val Val Leu Ala Leu Asp Pro Lys Gly His
 450 455 460
 Glu Asp Asp Ser Tyr Glu Ala Arg Lys Ser Phe Leu Thr Lys Tyr Phe
 465 470 475 480
 Asn Lys Gln Pro Tyr Pro Thr Arg Arg Glu Ile Glu Lys Leu Ala Ala
 485 490 495
 Ser Leu Trp Leu Trp Lys Ser Asp Ile Ala Ser His Phe Ser Asn Lys
 500 505 510
 Arg Lys Lys Cys Val Arg Asp Cys Glu Lys Tyr Lys Pro Gly Val Leu
 515 520 525
 Leu Gly Phe Asn Met Lys Glu Leu Asn Lys Val Lys His Glu Met Asp
 530 535 540
 Phe Asp Ala Glu Trp Leu Phe Glu Asn His Asp Glu Lys Asp Ser Arg
 545 550 555 560
 Val Asn Ala Ser Lys Thr Ala Asp Lys Lys Leu Asn Leu Gly Lys Glu
 565 570 575
 Asp Asp Ser Ser Ser Asp Ser Phe Glu Asn Leu Glu Glu Glu Ser Asn
 580 585 590
 Glu Ser Gly Ser Pro Phe Asp Pro Val Phe Glu Val Glu Pro Lys Ile
 595 600 605
 Ser Asn Asp Asn Pro Glu Glu His Val Leu Lys Val Ile Pro Glu Asp
 610 615 620
 Ala Ser Glu Ser Glu Glu Lys Leu Asp Gln Lys Glu Asp Gly Ser Lys
 625 630 635 640
 Tyr Glu Thr Ile His Leu Thr Glu Glu Pro Thr Lys Leu Met His Asn
 645 650 655
 Ala Ser Asp Ser Glu Val Asp Gln Asp Asp Val Val Glu Trp Lys Asp
 660 665 670
 Gly Ala Ser Pro Ser Glu Ser Gly Pro Gly Ser Gln Gln Val Ser Asp
 675 680 685
 Phe Glu Asp Asn Thr Cys Glu Met Lys Pro Gly Thr Trp Ser Asp Glu
 690 695 700
 Ser Ser Gln Ser Glu Asp Ala Arg Ser Ser Lys Pro Ala Ala Lys Lys
 705 710 715 720
 Lys Gly Tyr His Ala Arg
 725

<210> 58
 <211> 4193
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (492)..(3116)
 <223> H7 human activity dependent neurotrophic factor
 III (ADNF III) clone

<400> 58
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 ttctccttaa ttgcccctac tgtaccttca atgcagacaa aaagactttg gaaacacaca 180
 ttaaaatatt tcatgctccg aacgccagcg caccaagtag cagcttcagc actttcaaag 240
 ataaaaccaa aaatgatggc cttaaactta agcaggctga cagtgtagag caagctgttt 300
 attactgtaa gaagtgcact taccgagatc ctctttatga aatagttagg aagcacattt 360
 acagggaaca ttttcagcat gtggcagcac cttacatagc aaaggcagga gaaaaatcac 420
 tcaatggggc agtccccctta ggctcgaatg cccgagaaga gagtagtatt cactgcaagc 480
 gatgcctttt c atg cca aag tcc tat gaa gct ttg gta cag cat gtc atc 530
 Met Pro Lys Ser Tyr Glu Ala Leu Val Gln His Val Ile
 1 5 10
 gaa gac cat gaa cgt ata ggc tat cag gtc act gcc atg att ggg cac 578
 Glu Asp His Glu Arg Ile Gly Tyr Gln Val Thr Ala Met Ile Gly His
 15 20 25
 aca aat gta gtg gtt ccc cga tcc aaa ccc ttg atg cta att gct ccc 626
 Thr Asn Val Val Val Pro Arg Ser Lys Pro Leu Met Leu Ile Ala Pro
 30 35 40 45
 aaa cct caa gac aag aag agc atg gga ctc cca cca agg atc ggt tcc 674
 Lys Pro Gln Asp Lys Lys Ser Met Gly Leu Pro Pro Arg Ile Gly Ser
 50 55 60
 ctt gct tct gga aat gtc cgg tct tta cca tca cag cag atg gtg aat 722
 Leu Ala Ser Gly Asn Val Arg Ser Leu Pro Ser Gln Gln Met Val Asn
 65 70 75
 cga ctc tca ata cca aag cct aac tta aat tct aca gga gtc aac atg 770
 Arg Leu Ser Ile Pro Lys Pro Asn Leu Asn Ser Thr Gly Val Asn Met
 80 85 90
 atg tcc agt gtt cat ctg cag cag aac aac tat gga gtc aaa tct gta 818
 Met Ser Ser Val His Leu Gln Gln Asn Asn Tyr Gly Val Lys Ser Val
 95 100 105
 ggc cag ggt tac agt gtt ggt cag tca atg aga ctg ggt cta ggt ggc 866
 Gly Gln Gly Tyr Ser Val Gly Gln Ser Met Arg Leu Gly Leu Gly Gly
 110 115 120 125

aac gca cca gtt tcc att cct caa caa tct cag tct gta aag cag tta	914
Asn Ala Pro Val Ser Ile Pro Gln Gln Ser Gln Ser Val Lys Gln Leu	
130 135 140	
ctt cca agt gga aac gga agg tct tat ggg ctt ggg tca gag cag agg	962
Leu Pro Ser Gly Asn Gly Arg Ser Tyr Gly Leu Gly Ser Glu Gln Arg	
145 150 155	
tcc cag gca cca gca aga tac tcc ctg cag tct gct aat gcc tct tct	1010
Ser Gln Ala Pro Ala Arg Tyr Ser Leu Gln Ser Ala Asn Ala Ser Ser	
160 165 170	
ctc tca tcg ggc cag tta aag tct cct tcc ctc tct cag tca cag gca	1058
Leu Ser Ser Gly Gln Leu Lys Ser Pro Ser Leu Ser Gln Ser Gln Ala	
175 180 185	
tcc aga gtg tta ggt cag tcc agt tcc aaa cct gct gca gct gcc aca	1106
Ser Arg Val Leu Gly Gln Ser Ser Ser Lys Pro Ala Ala Ala Thr	
190 195 200 205	
ggc cct ccc cca ggt aac act tcc tca act caa aag tgg aaa ata tgt	1154
Gly Pro Pro Pro Gly Asn Thr Ser Ser Thr Gln Lys Trp Lys Ile Cys	
210 215 220	
aca atc tgt aat gag ctt ttt cct gaa aat gtc tat agt gtg cac ttc	1202
Thr Ile Cys Asn Glu Leu Phe Pro Glu Asn Val Tyr Ser Val His Phe	
225 230 235	
gaa aaa gaa cat aaa gct gag aaa gtc cca gca gta gcc aac tac att	1250
Glu Lys Glu His Lys Ala Glu Lys Val Pro Ala Val Ala Asn Tyr Ile	
240 245 250	
atg aaa ata cac aat ttt act agc aaa tgc ctc tac tgt aat cgc tat	1298
Met Lys Ile His Asn Phe Thr Ser Lys Cys Leu Tyr Cys Asn Arg Tyr	
255 260 265	
tta ccc aca gat act ctg ctc aac cat atg tta att cat ggt ctg tct	1346
Leu Pro Thr Asp Thr Leu Leu Asn His Met Leu Ile His Gly Leu Ser	
270 275 280 285	
tgt cca tat tgc cgt tca act ttc aat gat gtg gaa aag atg gcc gca	1394
Cys Pro Tyr Cys Arg Ser Thr Phe Asn Asp Val Glu Lys Met Ala Ala	
290 295 300	
cac atg cgg atg gtt cac att gat gaa gag atg gga cct aaa aca gat	1442
His Met Arg Met Val His Ile Asp Glu Glu Met Gly Pro Lys Thr Asp	
305 310 315	
tct act ttg agt ttt gat ttg aca ttg cag cag ggt agt cac act aac	1490
Ser Thr Leu Ser Phe Asp Leu Thr Leu Gln Gln Gly Ser His Thr Asn	
320 325 330	
atc cat ctc ctg gta act aca tac aat ctg agg gat gcc cca gct gaa	1538
Ile His Leu Leu Val Thr Thr Tyr Asn Leu Arg Asp Ala Pro Ala Glu	
335 340 345	
tct gtt gct tac cat gcc caa aat aat cct cca gtt cct cca aag cca	1586
Ser Val Ala Tyr His Ala Gln Asn Asn Pro Pro Val Pro Pro Lys Pro	
350 355 360 365	

cag cca aag gtt cag gaa aag gca gat atc cct gta aaa agt tca cct	1634
Gln Pro Lys Val Gln Glu Lys Ala Asp Ile Pro Val Lys Ser Ser Pro	
370 375 380	
caa gct gca gtg ccc tat aaa aaa gat gtt ggg aaa acc ctt tgt cct	1682
Gln Ala Ala Val Pro Tyr Lys Lys Asp Val Gly Lys Thr Leu Cys Pro	
385 390 395	
ctt tgc ttt tca atc cta aaa gga ccc ata tct gat gca ctt gca cat	1730
Leu Cys Phe Ser Ile Leu Lys Gly Pro Ile Ser Asp Ala Leu Ala His	
400 405 410	
cac tta cga gag agg cac caa gtt att cag acg gtt cat cca gtt gag	1778
His Leu Arg Glu Arg His Gln Val Ile Gln Thr Val His Pro Val Glu	
415 420 425	
aaa aag ctc acc tac aaa tgt atc cat tgc ctt ggt gtg tat acc agc	1826
Lys Lys Leu Thr Tyr Lys Cys Ile His Cys Leu Gly Val Tyr Thr Ser	
430 435 440 445	
aac atg acc gcc tca act atc act ctg cat cta gtt cac tgc agg ggc	1874
Asn Met Thr Ala Ser Thr Ile Thr Leu His Leu Val His Cys Arg Gly	
450 455 460	
gtt gga aag acc caa aat ggc cag gat aag aca aat gca ccc tct cgg	1922
Val Gly Lys Thr Gln Asn Gly Gln Asp Lys Thr Asn Ala Pro Ser Arg	
465 470 475	
ctt aat cag tct cca agt ctg gca cct gtg aag cgc act tac gag caa	1970
Leu Asn Gln Ser Pro Ser Leu Ala Pro Val Lys Arg Thr Tyr Glu Gln	
480 485 490	
atg gaa ttt ccc tta ctg aaa aaa cga aag tta gat gat gat agt gat	2018
Met Glu Phe Pro Leu Leu Lys Lys Arg Lys Leu Asp Asp Asp Ser Asp	
495 500 505	
tca ccc agc ttc ttt gaa gag aag cct gaa gag cct gtt gtt tta gct	2066
Ser Pro Ser Phe Phe Glu Glu Lys Pro Glu Glu Pro Val Val Leu Ala	
510 515 520 525	
tta gac ccc aag ggt cat gaa gat gat tcc tat gaa gcc agg aaa agc	2114
Leu Asp Pro Lys Gly His Glu Asp Asp Ser Tyr Glu Ala Arg Lys Ser	
530 535 540	
ttt cta aca aag tat ttc aac aaa cag ccc tat ccc acc agg aga gaa	2162
Phe Leu Thr Lys Tyr Phe Asn Lys Gln Pro Tyr Pro Thr Arg Arg Glu	
545 550 555	
att gag aag cta gca gcc agt tta tgg tta tgg aag agt gac atc gct	2210
Ile Glu Lys Leu Ala Ala Ser Leu Trp Leu Trp Lys Ser Asp Ile Ala	
560 565 570	
tcc cat ttt agt aac aaa agg aag aag tgt gtc cgt gat tgt gaa aag	2258
Ser His Phe Ser Asn Lys Arg Lys Lys Cys Val Arg Asp Cys Glu Lys	
575 580 585	
tac aag cct ggc gtg ttg ctg ggg ttt aac atg aaa gaa tta aat aaa	2306
Tyr Lys Pro Gly Val Leu Leu Gly Phe Asn Met Lys Glu Leu Asn Lys	
590 595 600 605	

gtc aag cat gag atg gat ttt gat gct gag tgg cta ttt gaa aat cat	2354
Val Lys His Glu Met Asp Phe Asp Ala Glu Trp Leu Phe Glu Asn His	
610 615 620	
gat gag aag gat tcc aga gtc aat gct agt aag act gct gac aaa aag	2402
Asp Glu Lys Asp Ser Arg Val Asn Ala Ser Lys Thr Ala Asp Lys Lys	
625 630 635	
ctc aac ctt ggg aag gaa gat gac agt tcc tca gac agt ttt gaa aat	2450
Leu Asn Leu Gly Lys Glu Asp Asp Ser Ser Ser Asp Ser Phe Glu Asn	
640 645 650	
ttg gaa gaa gaa tcc aat gaa agt ggt agc cct ttt gac cct gtt ttt	2498
Leu Glu Glu Glu Ser Asn Glu Ser Gly Ser Pro Phe Asp Pro Val Phe	
655 660 665	
gaa gtt gaa cct aaa atc tct aac gat aac cca gaa gaa cat gta ctg	2546
Glu Val Glu Pro Lys Ile Ser Asn Asp Asn Pro Glu Glu His Val Leu	
670 675 680 685	
aag gta att cct gag gat gct tca gaa tct gag gag aag cta gac caa	2594
Lys Val Ile Pro Glu Asp Ala Ser Glu Ser Glu Glu Lys Leu Asp Gln	
690 695 700	
aaa gaa gat ggt tca aaa tac gaa act att cat ttg act gag gaa cca	2642
Lys Glu Asp Gly Ser Lys Tyr Glu Thr Ile His Leu Thr Glu Glu Pro	
705 710 715	
acc aaa cta atg cac aat gca tct gat agt gag gtt gac caa gac gat	2690
Thr Lys Leu Met His Asn Ala Ser Asp Ser Glu Val Asp Gln Asp Asp	
720 725 730	
gtt gtt gag tgg aaa gac ggt gct tct cca tct gag agt ggg cct gga	2738
Val Val Glu Trp Lys Asp Gly Ala Ser Pro Ser Glu Ser Gly Pro Gly	
735 740 745	
tcc caa caa gtg tca gac ttt gag gac aat acc tgc gaa atg aaa cca	2786
Ser Gln Gln Val Ser Asp Phe Glu Asp Asn Thr Cys Glu Met Lys Pro	
750 755 760 765	
gga acc tgg tct gac gag tct tcc caa agc gaa gat gca agg agc agt	2834
Gly Thr Trp Ser Asp Glu Ser Ser Gln Ser Glu Asp Ala Arg Ser Ser	
770 775 780	
aag cca gct gcc aaa aaa aag gct acc atg caa ggt gac aga gag cag	2882
Lys Pro Ala Ala Lys Lys Lys Ala Thr Met Gln Gly Asp Arg Glu Gln	
785 790 795	
ttg aaa tgg aag aat agt tcc tat gga aaa gtt gaa ggg ttt tgg tct	2930
Leu Lys Trp Lys Asn Ser Ser Tyr Gly Lys Val Glu Gly Phe Trp Ser	
800 805 810	
aag gac cag tca cag tgg aag aat gca tct gag aat gat gag cgc tta	2978
Lys Asp Gln Ser Gln Trp Lys Asn Ala Ser Glu Asn Asp Glu Arg Leu	
815 820 825	
tct aac ccc cag att gag tgg cag aat agc aca att gac agt gag gat	3026
Ser Asn Pro Gln Ile Glu Trp Gln Asn Ser Thr Ile Asp Ser Glu Asp	
830 835 840 845	

ggg gaa cag ttt gac aac atg act gat gga gta gct gag ccc atg cat 3074
 Gly Glu Gln Phe Asp Asn Met Thr Asp Gly Val Ala Glu Pro Met His
 850 855 860

ggc agc tta gcc gga gtt aaa ctg agc agc caa cag gcc taagtgccag 3123
 Gly Ser Leu Ala Gly Val Lys Leu Ser Ser Gln Gln Ala
 865 870

gttccctggc attggtgaca tgctgcagcc tggaactctg atctccagtg tgactgcaaa 3183

gctgtcttct cactggtact gccttgtgag tactggttgg actgtggggc atgtggccgc 3243

tgcagttcca gtggttattt ctaagtctat gacaggacag gctgttcttg cttcagaacc 3303

ttctctgaca gacacggtaa ctaaagtga aaaaccaata agctggtgac tcatgaatac 3363

acacgaggaa aagcagaggt ttattttatc tgccttttca acatttcttt ccctctgtga 3423

aatgattggt cagatgtctt tgagaagtgt taaactaatt cacatggtag tgtagggcca 3483

acatacaagc taccagtcta atgtgtatag tagactttgg gaaaagcgat tttttttcat 3543

gtattcattc tgaatagttg aaatgtatat ttgtacagtc ttttagacct attcaagtga 3603

tgctcatgat cctgttactg tgtgccatc atagatttct ttttttagtg ttgcccttgc 3663

tgtgtaataa acgctctatc tagtttacct agcaaaagct caaaactgcy ctagtatgga 3723

ctttttggac agacttagtt tttgcacata acctgtgaca atcttgcaac agaggccagc 3783

cacgtaagat atatatctgg actctcttgg attataggat ttttcttggc ctgaatatcc 3843

ttgacattac agctgtcaaa aacaaaaact ggtatttcag atctgttttc tgaaatcttt 3903

taagctaaaa tcacatgcaa gaattgactt tgcagctact aattttgaca ctttttagat 3963

ctgtataaaa gtgtgttgtg ttgaagcagc aaaccaatga gtgctgcatt ttggatatat 4023

agttttatct ttagttcaac accatcatgg tggattcatt tataccatct aatatatgac 4083

acactgttgt agtatgtata attttgtgat ctttattttc cttttgtatt cattttaagc 4143

atctaaataa attgctgtat tgtgcttaat gtaaaaaaaaa aaaaaaaaaa 4193

<210> 59

<211> 874

<212> PRT

<213> Homo sapiens

<400> 59

Met Pro Lys Ser Tyr Glu Ala Leu Val Gln His Val Ile Glu Asp His
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Glu Arg Ile Gly Tyr Gln Val Thr Ala Met Ile Gly His Thr Asn Val
 20 25 30

Val Val Pro Arg Ser Lys Pro Leu Met Leu Ile Ala Pro Lys Pro Gln
 35 40 45

Asp Lys Lys Ser Met Gly Leu Pro Pro Arg Ile Gly Ser Leu Ala Ser
 50 55 60
 Gly Asn Val Arg Ser Leu Pro Ser Gln Gln Met Val Asn Arg Leu Ser
 65 70 75 80
 Ile Pro Lys Pro Asn Leu Asn Ser Thr Gly Val Asn Met Met Ser Ser
 85 90 95
 Val His Leu Gln Gln Asn Asn Tyr Gly Val Lys Ser Val Gly Gln Gly
 100 105 110
 Tyr Ser Val Gly Gln Ser Met Arg Leu Gly Leu Gly Gly Asn Ala Pro
 115 120 125
 Val Ser Ile Pro Gln Gln Ser Gln Ser Val Lys Gln Leu Leu Pro Ser
 130 135 140
 Gly Asn Gly Arg Ser Tyr Gly Leu Gly Ser Glu Gln Arg Ser Gln Ala
 145 150 155 160
 Pro Ala Arg Tyr Ser Leu Gln Ser Ala Asn Ala Ser Ser Leu Ser Ser
 165 170 175
 Gly Gln Leu Lys Ser Pro Ser Leu Ser Gln Ser Gln Ala Ser Arg Val
 180 185 190
 Leu Gly Gln Ser Ser Ser Lys Pro Ala Ala Ala Ala Thr Gly Pro Pro
 195 200 205
 Pro Gly Asn Thr Ser Ser Thr Gln Lys Trp Lys Ile Cys Thr Ile Cys
 210 215 220
 Asn Glu Leu Phe Pro Glu Asn Val Tyr Ser Val His Phe Glu Lys Glu
 225 230 235 240
 His Lys Ala Glu Lys Val Pro Ala Val Ala Asn Tyr Ile Met Lys Ile
 245 250 255
 His Asn Phe Thr Ser Lys Cys Leu Tyr Cys Asn Arg Tyr Leu Pro Thr
 260 265 270
 Asp Thr Leu Leu Asn His Met Leu Ile His Gly Leu Ser Cys Pro Tyr
 275 280 285
 Cys Arg Ser Thr Phe Asn Asp Val Glu Lys Met Ala Ala His Met Arg
 290 295 300
 Met Val His Ile Asp Glu Glu Met Gly Pro Lys Thr Asp Ser Thr Leu
 305 310 315 320
 Ser Phe Asp Leu Thr Leu Gln Gln Gly Ser His Thr Asn Ile His Leu
 325 330 335
 Leu Val Thr Thr Tyr Asn Leu Arg Asp Ala Pro Ala Glu Ser Val Ala
 340 345 350
 Tyr His Ala Gln Asn Asn Pro Pro Val Pro Pro Lys Pro Gln Pro Lys
 355 360 365

Val Gln Glu Lys Ala Asp Ile Pro Val Lys Ser Ser Pro Gln Ala Ala
 370 375 380
 Val Pro Tyr Lys Lys Asp Val Gly Lys Thr Leu Cys Pro Leu Cys Phe
 385 390 395 400
 Ser Ile Leu Lys Gly Pro Ile Ser Asp Ala Leu Ala His His Leu Arg
 405 410 415
 Glu Arg His Gln Val Ile Gln Thr Val His Pro Val Glu Lys Lys Leu
 420 425 430
 Thr Tyr Lys Cys Ile His Cys Leu Gly Val Tyr Thr Ser Asn Met Thr
 435 440 445
 Ala Ser Thr Ile Thr Leu His Leu Val His Cys Arg Gly Val Gly Lys
 450 455 460
 Thr Gln Asn Gly Gln Asp Lys Thr Asn Ala Pro Ser Arg Leu Asn Gln
 465 470 475 480
 Ser Pro Ser Leu Ala Pro Val Lys Arg Thr Tyr Glu Gln Met Glu Phe
 485 490 495
 Pro Leu Leu Lys Lys Arg Lys Leu Asp Asp Asp Ser Asp Ser Pro Ser
 500 505 510
 Phe Phe Glu Glu Lys Pro Glu Glu Pro Val Val Leu Ala Leu Asp Pro
 515 520 525
 Lys Gly His Glu Asp Asp Ser Tyr Glu Ala Arg Lys Ser Phe Leu Thr
 530 535 540
 Lys Tyr Phe Asn Lys Gln Pro Tyr Pro Thr Arg Arg Glu Ile Glu Lys
 545 550 555 560
 Leu Ala Ala Ser Leu Trp Leu Trp Lys Ser Asp Ile Ala Ser His Phe
 565 570 575
 Ser Asn Lys Arg Lys Lys Cys Val Arg Asp Cys Glu Lys Tyr Lys Pro
 580 585 590
 Gly Val Leu Leu Gly Phe Asn Met Lys Glu Leu Asn Lys Val Lys His
 595 600 605
 Glu Met Asp Phe Asp Ala Glu Trp Leu Phe Glu Asn His Asp Glu Lys
 610 615 620
 Asp Ser Arg Val Asn Ala Ser Lys Thr Ala Asp Lys Lys Leu Asn Leu
 625 630 635 640
 Gly Lys Glu Asp Asp Ser Ser Ser Asp Ser Phe Glu Asn Leu Glu Glu
 645 650 655
 Glu Ser Asn Glu Ser Gly Ser Pro Phe Asp Pro Val Phe Glu Val Glu
 660 665 670
 Pro Lys Ile Ser Asn Asp Asn Pro Glu Glu His Val Leu Lys Val Ile
 675 680 685

Pro Glu Asp Ala Ser Glu Ser Glu Glu Lys Leu Asp Gln Lys Glu Asp
 690 695 700
 Gly Ser Lys Tyr Glu Thr Ile His Leu Thr Glu Glu Pro Thr Lys Leu
 705 710 715 720
 Met His Asn Ala Ser Asp Ser Glu Val Asp Gln Asp Asp Val Val Glu
 725 730 735
 Trp Lys Asp Gly Ala Ser Pro Ser Glu Ser Gly Pro Gly Ser Gln Gln
 740 745 750
 Val Ser Asp Phe Glu Asp Asn Thr Cys Glu Met Lys Pro Gly Thr Trp
 755 760 765
 Ser Asp Glu Ser Ser Gln Ser Glu Asp Ala Arg Ser Ser Lys Pro Ala
 770 775 780
 Ala Lys Lys Lys Ala Thr Met Gln Gly Asp Arg Glu Gln Leu Lys Trp
 785 790 795 800
 Lys Asn Ser Ser Tyr Gly Lys Val Glu Gly Phe Trp Ser Lys Asp Gln
 805 810 815
 Ser Gln Trp Lys Asn Ala Ser Glu Asn Asp Glu Arg Leu Ser Asn Pro
 820 825 830
 Gln Ile Glu Trp Gln Asn Ser Thr Ile Asp Ser Glu Asp Gly Glu Gln
 835 840 845
 Phe Asp Asn Met Thr Asp Gly Val Ala Glu Pro Met His Gly Ser Leu
 850 855 860
 Ala Gly Val Lys Leu Ser Ser Gln Gln Ala
 865 870

<210> 60

<211> 482

<212> DNA

<213> Mus musculus

<220>

<221> promoter

<222> (1)..(482)

<223> mouse activity dependent neurotrophic factor III
 (ADNF III) promoter

<400> 60

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tgcattgcaa cagtgtcacc tgtgagttcc tgtgtctgaa gccgagaaga tccacaaaat 120

gaggcttttc catagttggt ttgtgttttt aacaagaaaa tggagaggct ttttgtttgt 180

ttttgttttt gtttttttgc ctctgacttc tctctgaaac cagccaacaa gtacaactag 240

caatttttaa agatttagca agaacttgca ctgagttttc atttacagga gcacaaataa 300

aaatatttga ttcaaaaatg catctgagtt cttttaattt ttcctgcagg agaaacctct 360

aaaagtcatt gccttgacaga gtttctggga atgcctgggg gagggagcctg gaacttgtaa 420
 ctgcttgccct tgagtggcct tctcactctg gtttctgttc tgttttgttt cgtttgtttt 480
 tt 482

<210> 61
 <211> 50
 <212> DNA
 <213> Homo sapiens

<220>
 <223> H6, H7 and H2 clone human activity dependent
 neurotrophic factor III (ADNF III) polymorphic
 region

<220>
 <221> variation
 <222> (47)
 <223> polymorphic site a -> g transition

<400> 61
 gagttaaact gagcagccaa caggcctaag tgccagggttc cctggcattg 50

<210> 62
 <211> 50
 <212> DNA
 <213> Homo sapiens

<220>
 <223> H10 clone human activity dependent neurotrophic
 factor III (ADNF III) polymorphic region

<220>
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 <222> (13)
 <223> n = unknown

<220>
 <221> modified_base
 <222> (16)
 <223> n = unknown

<220>
 <221> modified_base
 <222> (20)
 <223> n = unknown

<220>
 <221> modified_base
 <222> (40)
 <223> n = unknown

<220>
 <221> variation
 <222> (47)
 <223> polymorphic site a -> g transition

<400> 62
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<210> 63
<211> 50
<212> DNA
<213> Homo sapiens

<220>
<223> H3, H12 and H4 clone human activity dependent
neurotrophic factor III (ADNF III) polymorphic
region

<220>
<221> variation
<222> ()
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<400> 63
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